I CLAIM:

1. A method of creating a prognosis protocol for a patient diagnosed with a neurological disease, said method comprising:

a) identifying a patient already diagnosed with said disease;

b) determining the apoE allele load of said patient; and

c) converting the data obtained from step b) into a prognosis protocol, said prognosis protocol including a prediction of drug efficacy and patient outcome.

2. A method of creating a prognosis protocol for a patient diagnosed with AD, said method comprising:

a) identifying a patient already diagnosed with said disease;

b) determining the apoE allele load of said patient; and

c) converting the data obtained from steps b) and c) into a prognosis protocol, said prognosis protocol including a prediction of drug efficacy and patient outcome.

3. The method of claim 1 or claim 2, wherein said method further comprises obtaining a patient profile.

4. The method of claim 1, wherein said patient is diagnosed with a disease selected from the group consisting of: prion diseases, a pathology of the developing nervous system, a pathology of the aging nervous system, nervous system injury, coma, infection of the nervous system, dietary deficiency, and cardiovascular injury.

5. The method of claim 4, wherein said prion disease is Creutzfeldt-Jakob disease.

6. The method of claim 4, wherein said patient is diagnosed with a congenital defect in amino acid metabolism.

7. The method of claim 6, wherein the defect is selected for the group consisting of arginosuccinic aciduria, cystathionuria, histidinaemia, homocystinuria, hyperammonaemia, phenylketonuria, and tyrosinanaemia.

8. The method of claim 4, wherein said patient is diagnosed with fragile X syndrome.

9. The method of claim 4, wherein said patient diagnosed with disease selected from the group consisting of neurofibromatosis, Huntington's disease, depression, amyotrophic lateral sclerosis, multiple sclerosis, stroke, Parkinson's disease and multiple infarcts dementia.

10. The method of claim 9, wherein said disease is Alzheimer's disease.

11. The method of claim 3, wherein said patient profile includes a determination of said patient's sex.

~~12. The method of claim 3, wherein said patient profile includes the genotype of said patient.~~

13. The method of claim 12, wherein said genotype is the presenilin genotype.

14. The method of claim 12, wherein said genotype is the apolipoprotein C1 genotype.

15. A method for identifying non-AD patients for participation in clinical trail of a drug for the treatment of a non-AD neurological disease, said method compromising:

a) identifying a patient already diagnosed with said non-AD neurological disease;

b) determining the *apoE* allele load of said patient; and

c) converting the data obtained from step b into a prognosis protocol, said prognosis protocol indicating whether or not said patient is a candidate for a cholinomimetic drug trial or non-cholinomimetic drug trial.

16. A method for identifying AD patients for participation in clinical trail of a drug for the treatment of an AD, said method compromising:

a) identifying a patient already diagnosed with said AD;

b) determining the *apoE* allele load of said patient; and

c) converting the data obtained from step b into a prognosis protocol, said prognosis protocol indicating whether or not said patient is a candidate for a cholimomenetic drug trial or non-cholimometic drug trial.

17. A method for determining whether a human will respond to cholinomimetic cognitive enhancer, said method comprising:

a) obtaining a patient profile on said human;

b) determining the *apoE* allele load of said human; and

c) selecting those humans having at least one *apoE2* or *apoE3* allele as recipients of said cholinomimetic drug.

18. A kit for performing pharmacogenetic analysis, said kit including a means for converting the patient profile into a prognosis protocol.

19. The kit of claim 15, wherein said kit contains a means for performing the steps of said conversion.

20. The kit of claim 15, wherein said kit contains a means for compiling the data for said patient profile.